

CLONING AND USES OF THE GENETIC LOCUS bcl-6

5 The invention disclosed herein was made with Government support under NIH Grant Nos. CA-44029, CA-34775, CA-08748 and CA-37295 from the Department of Health and Human Services. Accordingly, the U.S. Government has certain rights in this invention.

10 This application is a continuation-in-part of United States application Serial No. 08/074,967, filed on June 9, 1993, the contents of which are hereby incorporated by reference.

15 BACKGROUND OF THE INVENTION

Throughout this application various references are referred to within parenthesis. Disclosures of these publications in their entireties are hereby incorporated by reference into this application to more fully describe the state of the art to which this invention pertains. Full bibliographic citation for these references may be found at the end of each Experimental Detail Section.

25 Non-random chromosomal abnormalities are found in up to 90% of patients with non-Hodgkin's lymphoma (NHL) and have been shown to play an important role in lymphomagenesis by activating proto-oncogenes (1). Some of these translocations, which are associated with specific histologic subsets of NHL, have been characterized at the molecular level. In the t(8;14), t(8;22), and t(2;8) translocations associated with Burkitt Lymphoma, L₃-type acute lymphoblastic leukemia and AIDS-associated non-Hodgkin lymphoma (NHL), a known proto-oncogene, c-myc, was found juxtaposed to the immunoglobulin (Ig) loci (2,3). In the t(14;18) translocation, which is implicated in follicular-type NHL, molecular analysis of the sequences linked to the Ig locus led to the identification of a novel proto-

oncogene, bcl-2 (4-6). The t(11;14)(q13;q32), mainly associated with "mantle zone" lymphoma, appears to involve the juxtaposition of the Ig heavy-chain locus with the bcl-1 locus, the site of the candidate proto-oncogene PRAD-1/cyclin D1 (7,8). These well characterized chromosome translocations are associated, however, with only a fraction of NHL cases, while a number of other recurrent translocations remain to be characterized for their genetic components.

One important example of such cytogenetic abnormalities is represented by various alterations affecting band 3q27. This region is involved in translocations with various chromosomal sites including, but not limited, to those carrying the Ig heavy- (14q32) or light- (2p12, 22q11) chain loci (9,10). Overall, 3q27 breakpoints are detectable in 7-12% of B-cell NHL cases by cytogenetic analysis, with t(3;22)(q27;q11) being the most frequent type detectable in 4-5% of NHL (9). The clinicopathologic relevance of 3q27 breakpoints is underscored by its consistent association with diffuse-type NHL, a frequent and clinical aggressive subtype for which no specific molecular lesion has yet been identified (9).

The recurrence of 3q27 breakpoints in NHL has prompted a search for the corresponding proto-oncogene. This invention discloses the cloning of clustered 3q27 breakpoints from two NHL cases carrying t(3;14)(q27;q32) translocations and the identification of genomic rearrangements within the same breakpoint region in additional NHL cases carrying translocations involving 3q27. Within the same region, a transcriptional unit has been identified, which represents the candidate proto-oncogene (bcl-6) associated with 3q27 translocations in B-NHL.

SUMMARY OF THE INVENTION

This invention provides an isolated vertebrate nucleic acid molecule of bcl-6 locus. This invention provides
5 an isolated vertebrate DNA molecule of bcl-6 locus. This invention provides an isolated vertebrate cDNA molecule of bcl-6. This invention provides an isolated genomic DNA molecule of bcl-6. This invention provides an isolated vertebrate RNA molecule of bcl-6. This
10 invention provides an isolated human nucleic acid molecule of bcl-6 locus.

In addition, this invention provides a nucleic acid molecule comprising a nucleic acid molecule of at least
15 15 nucleotides capable of specifically hybridizing with a sequence included within the sequence of the nucleic acid molecule of bcl-6.

In addition, this invention provides an isolated
20 vertebrate DNA molecule of bcl-6 operatively linked to a promoter of RNA transcription. This invention provides a vector which comprises the isolated vertebrate DNA molecule of bcl-6.

25 In addition, this invention provides the above vector, wherein the isolated nucleic acid molecule is linked to a plasmid.

30 In addition, this invention provides a host vector system for the production of a polypeptide encoded by bcl-6 locus, which comprises the above vector in a suitable host.

35 In addition, this invention provides a method of producing a polypeptide encoded by bcl-6 locus, which comprises growing the above host vector system under suitable conditions permitting production of the

polypeptide and recovering the polypeptide so produced.

5 In addition, this invention provides a polypeptide encoded by the isolated vertebrate nucleic acid molecule of bcl-6 locus. Further, this invention provides an antibody capable of binding to polypeptide encoded by bcl-6 locus.

10 In addition, this invention provides an antagonist capable of blocking the expression of the polypeptide encoded by bcl-6.

15 In addition, this invention provides an antisense molecule capable of hybridizing to the nucleic acid molecule of bcl-6.

20 In addition, this invention provides an assay for non-Hodgkin's lymphoma, a method for screening putative therapeutic agents for treatment of non-Hodgkin's lymphoma and a method for diagnosing B-cell lymphoma.

Finally, this invention provides a method of treating a subject with non-Hodgkin's lymphoma.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1: Immunoglobulin gene rearrangement analysis of KC1445 and SM1444 DNA. DNA extracted from the cell lines U937 (monocytic leukemia) and SK-N-MC (neuroblastoma) were used as controls for non-rearranged, germ-line Ig genes. In the left panel, the arrow on the left points to the rearranged J_H fragment which does not contain C_μ sequences in KC1445 DNA, while the two arrows on the right point to the two distinct fragments containing J_H or C_μ sequences in SM1444 DNA.

Figure 2: Molecular cloning of the chromosomal breakpoints from two NHL cases with t(3;14). Illustrated are the maps of two representative phage clones spanning the breakpoint regions in case SM1444 (SM-71) and KC1445 (KC-51). Chromosome 14 portions of the phage inserts are indicated by a solid line with hatched and black boxes representing switch sequences and C_μ exons, respectively. Vertical arrows point to the junctions of chromosome 3 and 14 sequences. The probes used for Southern (Figure 4) and Northern (Figure 5) analysis are illustrated below the SM-71 map. Restriction enzyme sites are indicated as: B=BamHI; H=HindIII; R=EcoRI; G=BglIII; S=sacI.

Figure 3: Localization of phage SM-71 sequences to chromosomes 3 and 14 by fluorescence

in situ hybridization. Consistent hybridization signals at 3q27 (arrow in panel A) and 14q32 (arrow in panel B) demonstrated that the insert is derived from the translocation junction.

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Figures 4A-4C: Southern blot hybridization analysis of bcl-6 rearrangements in NHL carrying 3q27 breakpoints. The probes used are illustrated in Figure 2. U937 and SK-N-MC DNAs are used as germ-line controls since their hybridization pattern was identical to the one observed in a panel of 19 control DNAs tested. The detected cytogenetic abnormalities affecting 3q27 in each case are: KC1445: t(3;14)(q27;q32); SM1444: t(3;14)(q27;q32); TF1403: t(3;14)(q27;q32); LD1411: t(3,14)(q27;q32); EM352: t(3;22)(q27;q11); CF755: t(3;12)(q27;q11); S0955:der(3)t(3;5)(q27;q31).

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Figure 5: Identification of the bcl-6 transcriptional unit. 15 µg of total RNA isolated from the indicated human cell lines was analyzed by Northern blot hybridization using the Sac 4.0 probe (see Figure 2). CB33:EBV-immortalized human B lymphoblastoid cell line; HeLa: human cervical carcinoma cell line; Daudi: human Burkitt lymphoma cell line; Hut78: human T-cell leukemia cell line. Hybridization of the same filter to a mouse GAPDH probe is shown as control

for RNA amount loaded in each lane. The faint band comigrating with 28S RNA in all the lanes may be the result of cross-hybridization with ribosomal RNA sequences.

Figure 6: Map of normal human BCL-6 locus. A recombinant genomic DNA library derived from normal placenta DNA was obtained from STRATAGENE Inc and screened by plaque hybridization using the Sac 4.0 probe. Three recombinant phages were obtained (ϕ 1-3 in the figure) whose inserts have been mapped and shown to overlap on approximately 30 kilobases of genomic DNA representing the BCL-6 locus. These sequences containing bcl-6 exons since they hybridize to the cDNA probe. The precise position of the exons has only been approximately determined and is schematically indicated in the figure. The position of the breakpoints observed in various lymphoma cases is also indicated.

Figure 7: pSac 40 plasmid construction.

Figure 8: pGB31 and pGB3s plasmid construction.

Figures 9A-9D: cDNA and Amino Acid Sequences of BCL-6 (SEQ ID NOs. 1 and 2). The Sac 4.0 probe was used to screen a recombinant phage cDNA library constructed from Bjab B cell lymphoma line RNA. A 4.0 kilobase cDNA was isolated and its nucleotide sequence was determined. It contains a long open reading frame

5 potentially coding for 706 amino acid protein which contains five zinc-finger domains (underlined in the figure; C and H residues which identify the C2H2-type zinc-finger structure are indicated in bold).

Figures 10A-10B:

10 Structure of BCL-6 cDNA and sequence of its predicted protein product. Figure 10A: Schematic representation of the full-length BCL-6 cDNA clone showing the relative position of the open reading frame (box) with 5' and 3' untranslated sequences (lines flanking the box). The approximate positions of the zinc-finger motifs (Zn++) and the NH₂-terminal homology (shaded area) with other proteins are also indicated.

15 Figure 10B: The predicted amino acid sequence of the BCL-6 protein. The residues corresponding to the six zinc-finger motifs (H-C links). The GenBank Accession number for BCL-6 cDNA and amino acid sequences is U00115.

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Figure 11: Homology of the NH₂-terminal region of BCL-6 to other Krüppel zinc-finger proteins, viral (VA55R), or cellular non-zinc-finger (kelch) proteins. Black background indicates identical residues found four or more times at a given position; grey indicates conserved residues that appear in at least four sequences at a given position. Conserved amino acid substitutions are defined according to

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scheme (P, A, G, S, T), (Q, N, E, D), (H, K, R), (L, I, V, M), and (F< Y< W). Numbering is with respect to the methionine initiation codon of each gene.

Figure 12:

Exon-intron organization of the BCL-6 gene and mapping of breakpoints detected in DLCL. Coding and non-coding exons are represented by filled and empty boxes, respectively. The position and size of each exon are approximate and have been determined by the pattern of hybridization of various cDNA probes as well as by the presence of shared restriction sites in the genomic and cDNA. The putative first, second and third exons have been sequenced in the portions overlapping the cloned cDNA sequences. The transcription initiation site has not been mapped (shaded box on 5' side of first exon). Patient codes (e.e. NC11, 891546 etc.) are grouped according to the rearranged patterns displayed by tumor samples. Arrows indicate the breakpoint position for each sample as determined by restriction enzyme/hybridization analysis. For samples KC1445 and SM1444, the breakpoints have been cloned and the precise positions are known. Restriction sites marked by asterisks have been only partially mapped within the BCL-6 locus. Restriction enzyme symbols are: S, Sac I; B, Bam HI; X, Xba I; H, Hind III; R, Eco RI; G, Bgl

II; P, Pst I; Sc, Sca I; St, Stu I; Rs, Rsa I. Tumor samples were collected and analyzed for histopathology at Memorial Sloan-Kettering Cancer Center or at Columbia University.

Figures 13A-13B:

Rearrangements of the BCL-6 gene in diffuse large-cell lymphomas (DLCL). Genomic DNA extracted from tumor biopsies of DLCL cases and from normal lymphocytes (lane N) was digested with the indicated restriction enzymes and analyzed by Southern blot hybridization using the Sac 4.0 probe. Abnormal restriction fragments are indicated by the arrows.

Figures 14A-14C:

Analysis of BCL-6 rearrangements in AIDS-NHL (Figures 14A-14C). DNAs were digested with BamHI (Figure 14A) or XbaI (Figures 14B and 14C) and hybridized to probes Sac4.0 (Figures 14A and 14B) or Sac0.8 (Figure 14C). The BCL-6 germline bands detected by BamHI (11.4 Kb) and XbaI (14 Kb) are indicated. U937 was used as a BCL-6 germline control. Among the cases shown, rearrangements were detected in cases DK782, DK827, and DS16, represented by AIDS-DLCL.

Figure 15:

Restriction map of the germline BCL-6 locus. Exon-intron organization of the BCL-6 gene. Coding and noncoding exons are represented by filled and empty boxes, respectively. The transcription

initiation site has not been mapped (shaded box on 5' side of first exon). The breakpoints detected in AIDS-NHL are indicated by arrows. Restriction enzyme symbols are: S, *SacI*; B, *BamHI*; X, *XbaI*, R, *EcoRI*. RE, restriction enzyme.

Figures 16A-16C:

10 Analysis of EBV infection (Figure 16A),
c-MYC rearrangements (Figure 16B), and
p53 mutations (Figure 16C) in AIDS-NHL.
Figure 16A: Analysis of EBV termini
heterogeneity in AIDS-NHL. DNAs were
15 digested with *BamHI* and subjected to
Southern hybridization using a DNA
probe specific for the fused termini of
the EBV genome. U937, a monocytic
leukemia cell line, is used as a
20 negative control. A lymphoblastoid
cell line derived by EBV infection of
normal polyclonal B cells (NC2) is used
as control for polymorphic EBV termini.
Representative samples of AIDS-NHL,
25 both positive (DK3794, DK4338, DK2814,
DK3973) and negative (DK3479), are
shown. Figure 16B: Southern blot
analysis of c-MYC rearrangements in
AIDS-NHL. Genomic DNAs from the cases
30 shown was digested with *HindIII* and
probed with clone MC413RC⁴¹,
representative of c-MYC exon 3. A
lymphoblastoid cell line (NC2) was used
as control for c-MYC germline
35 configuration. Among the cases shown,
two cases of AIDS-DLCL (DK3537 and
DK1446) display a c-MYC rearrangement.

Figure 16C: Analysis by PCR-SSCP of the p53 gene in AIDS-NHL. Representative examples are shown for p53 exon 5. Samples were scored as abnormal when differing from the normal control (N). A sample known to harbor a p53 mutation was used as positive control (POS). Among the cases shown, DK1171, a case of AIDS-SNCCCL, shows a p53 mutation which was further characterized by direct sequencing of the PCR product.

Figures 17A-17B:

Southern blot analysis of the BCL-6 gene configuration in diffuse large cell lymphomas. Genomic DNA extracted from tumor biopsies was digested with the indicated restriction endonucleases and hybridized using the Sac4.0 probe (19). Rearranged fragments are indicated by the arrows. N = normal control DNA obtained from human lymphocytes.

Figures 18A-18B:

Figure 18A: Freedom from progression in BCL-6 rearranged cases (open circles, top curve) compared to BCL-6 germline cases (closed circles, bottom curve) ($P=0.007$). Figure 18B: Overall survival from time of diagnosis for BCL-6 rearranged CLLC (open circle, top curve), compared to BCL-6 germline, BCL-2 germline DLLC (dark triangles, middle curve), and BCL-2 rearranged DLLC (dark boxes, bottom curve) ($P=0.02$).

DETAILED DESCRIPTION OF THE INVENTION

5 The following standard abbreviations are used throughout the specification to indicate specific nucleotides:

| | |
|-------------|-------------|
| C=cytosine | A=adenosine |
| T=thymidine | G=guanosine |

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This invention provides an isolated vertebrate nucleic acid molecule of the bcl-6 locus. As used herein, bcl-6 locus means the breakpoint cluster region in B-cell lymphomas. The bcl-6 locus is of 30 kilobase in length
15 containing at least a bcl-6 gene which codes for a protein. Therefore, the bcl-6 locus contains both the 5' and 3' flanking region of the coding sequences of the bcl-6 gene.

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In an embodiment, the isolated, vertebrate nucleic acid molecule of bcl-6 locus is DNA. In another embodiment, the isolated, vertebrate nucleic acid of the bcl-6 locus is cDNA. In a further embodiment, the isolated, vertebrate nucleic acid is genomic DNA. In a still
25 further embodiment, the isolated, vertebrate nucleic acid molecule is RNA.

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This invention provides an isolated, human nucleic acid molecule comprising the bcl-6 locus.

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The DNA molecules described and claimed herein are useful for the information which they provide concerning the amino acid sequence of the polypeptide and as products for the large scale synthesis of the polypeptide by a variety of recombinant techniques. The molecule is useful for generating new cloning and expression vectors, transformed and transfected

prokaryotic and eukaryotic host cells, and new and useful methods for cultured growth of such host cells capable of expression of the polypeptide and related products.

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Moreover, the isolated vertebrate nucleic acid molecules are useful for the development of probes to study B cell lymphomas.

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This invention provides a nucleic acid molecule comprising a nucleic acid molecule of at least 15 nucleotides capable of specifically hybridizing with a sequence included within the sequence of the bcl-6 locus. In an embodiment, this molecule is DNA. In another embodiment, the molecule is RNA.

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As used herein, the phrase "specifically hybridizing" means the ability of a nucleic acid molecule to recognize a nucleic acid sequence complementary to its own and to form double-helical segments through hydrogen bonding between complementary base pairs.

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The above nucleic acid molecule of at least 15 nucleotides capable of specifically hybridizing with a sequence of bcl-6 locus may be used as a probe for bcl-6 sequences. Nucleic acid probe technology is well known to those skilled in the art who will readily appreciate that such probes may vary greatly in length and may be labeled with a detectable label, such as a radioisotope or fluorescent dye, to facilitate detection of the probe. DNA probe molecules may be produced by insertion of a DNA molecule having the full-length or a fragment of the bcl-6 locus into suitable vectors, such as plasmids or bacteriophages, followed by transforming into suitable bacterial host cells, replication in the transformed bacterial host cells and harvesting of the DNA probes, using methods

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well known in the art. Alternatively, probes may be generated chemically from DNA synthesizers.

5 RNA probes may be generated by inserting the full length or a fragment of the bcl-6 locus downstream of a bacteriophage promoter such as T3, T7 or SP6. Large amounts of RNA probe may be produced by incubating the labeled nucleotides with a linearized bcl-6 or its
10 fragment where it contains an upstream promoter in the presence of the appropriate RNA polymerase.

This invention provides an cDNA molecule of bcl-6 locus operatively linked to a promoter of RNA transcription.

15 This invention provides a vector which comprises the nucleic acid molecule of bcl-6 locus. This invention provides the above vector, wherein the isolated nucleic acid molecule is linked to a plasmid.

20 This invention further provides isolated cDNA molecule of the bcl-6 locus operatively linked to a promoter of RNA transcription. Various vectors including plasmid vectors, cosmid vectors, bacteriophage vectors and other viruses are well known to ordinary skilled
25 practitioners.

As an example to obtain these vectors, insert and vector DNA can both be exposed to a restriction enzyme to create complementary ends on both molecules which
30 base pair with each other and are then ligated together with DNA ligase. Alternatively, linkers can be ligated to the insert DNA which correspond to a restriction site in the vector DNA, which is then digested with the restriction enzyme which cuts at that site. Other
35 means are also available and known to an ordinary skilled practitioner.

In an embodiment, a partial cDNA molecule of the bcl-6 locus is linked to pGEM-7zf(-) and the resulting plasmid is designated as pGB31 (Figure 8). Plasmid, pGB31 was deposited on June 3, 1993 with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland 20852, U.S.A. under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganism for the Purposes of Patent Procedure. Plasmid, pGB31 was
5
10 accorded with ATCC Accession Number 75476.

In an another embodiment, a partial cDNA molecule of the bcl-6 locus is linked to pGEM-7zf(-) and the resulting plasmid is designated as pGB3s (Figure 8). Plasmid, pGB3s was deposited on June 3, 1993 with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland 20852, U.S.A. under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganism for the Purposes of Patent Procedure. Plasmid, pGB3s was
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20 accorded with ATCC Accession Number 75477.

This invention provides a host vector system for the production of a polypeptide encoded by bcl-6 locus, which comprises the above vector in a suitable host.
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This invention provides the above host vector system, wherein the suitable host is a bacterial cell, insect cell, or animal cell.

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Regulatory elements required for expression include promoter sequences to bind RNA polymerase and transcription initiation sequences for ribosome binding. For example, a bacterial expression vector includes a promoter such as the lac promoter and for
35 transcription initiation the Shine-Dalgarno sequence and the start codon AUG. Similarly, a eukaryotic

expression vector includes a heterologous or homologous promoter for RNA polymerase II, a downstream polyadenylation signal, the start codon AUG, and a termination codon for detachment of the ribosome. Such
5 vectors may be obtained commercially or assembled from the sequences described by methods well-known in the art, for example the methods described above for constructing vectors in general. Expression vectors are useful to produce cells that express the
10 polypeptide encoded by the bcl-6 locus.

This invention further provides an isolated DNA or cDNA molecule described hereinabove wherein the host cell is selected from the group consisting of bacterial cells
15 (such as E.coli), yeast cells, fungal cells, insect cells and animal cells. Suitable animal cells include, but are not limited to Vero cells, HeLa cells, Cos cells, CV1 cells and various primary mammalian cells.

20 This invention provides a method of producing a polypeptide encoded by bcl-6 locus, which comprises growing the above host vector system under suitable conditions permitting production of the polypeptide and recovering the polypeptide so produced.

25 This invention provides a polypeptide encoded by the isolated vertebrate nucleic acid molecule of bcl-6 locus.

30 This invention provides an antibody capable of binding to polypeptide encoded by bcl-6 locus. In an embodiment, the antibody is monoclonal.

This invention provides a method to select specific
35 regions on the polypeptide encoded by the bcl-6 locus to generate antibodies. The protein sequence may be determined from the cDNA sequence. Amino acid

sequences may be analyzed by methods well known to those skilled in the art to determine whether they produce hydrophobic or hydrophilic regions in the proteins which they build. In the case of cell
5 membrane proteins, hydrophobic regions are well known to form the part of the protein that is inserted into the lipid bilayer of the cell membrane, while hydrophilic regions are located on the cell surface, in an aqueous environment. Usually, the hydrophilic
10 regions will be more immunogenic than the hydrophobic regions. Therefore the hydrophilic amino acid sequences may be selected and used to generate antibodies specific to polypeptide encoded by the bcl-6 locus. The selected peptides may be prepared using
15 commercially available machines. As an alternative, DNA, such as a cDNA or a fragment thereof, may be cloned and expressed and the resulting polypeptide recovered and used as an immunogen.

20 Polyclonal antibodies against these peptides may be produced by immunizing animals using the selected peptides. Monoclonal antibodies are prepared using hybridoma technology by fusing antibody producing B cells from immunized animals with myeloma cells and
25 selecting the resulting hybridoma cell line producing the desired antibody. Alternatively, monoclonal antibodies may be produced by in vitro techniques known to a person of ordinary skill in the art. These antibodies are useful to detect the expression of
30 polypeptide encoded by the bcl-6 locus in living animals, in humans, or in biological tissues or fluids isolated from animals or humans.

The antibody may be labelled with a detectable marker,
35 including but not limited to: a radioactive label, or a calorimetric, luminescent, or fluorescent marker, or gold. Radioactive labels include but are not limited

to: ³H, ¹⁴C, ³²P, ³³P; ³⁵S, ³⁶Cl, ⁵¹Cr, ⁵⁷Co, ⁵⁹Co, ⁵⁹Fe, ⁹⁰Y, ¹²⁵I, ¹³¹I, and ¹⁸⁶Re. Fluorescent markers include but are not limited to: fluorescein, rhodamine and auramine. Methods of producing the polyclonal or monoclonal
5 antibody are known to one of ordinary skill in the art.

Further, the antibody complex may be detected by a second antibody which may be linked to an enzyme, such as alkaline phosphatase or horseradish peroxidase.
10 Other enzymes which may be employed are well known to one of ordinary skill in the art.

This invention provides for the isolated nucleic acid molecule of bcl-6 that is labelled with a detectable
15 marker. The detectable marker may be a radioactive label, a calorimetric, luminescent, or a fluorescent marker. Other detectable markers are known to those skilled in the art as hereinabove described.

This invention provides an antagonist capable of blocking the expression of the polypeptide encoded by the isolated nucleic acid molecule of bcl-6. The antagonist may be a triplex oligonucleotide capable of hybridizing to nucleic acid molecule bcl-6.
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25 This invention provides an antisense molecule capable of hybridizing to the nucleic acid molecule bcl-6. The antisense molecule may be DNA or RNA.

30 This invention provides a triplex oligonucleotide capable of hybridizing with a double stranded DNA molecule bcl-6.

The antisense molecule may be DNA or RNA or variants thereof (i.e. DNA with a protein backbone). The present invention extends to the preparation of antisense nucleotides and ribozymes that may be used to
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interfere with the expression of the receptor recognition proteins at the translation of a specific mRNA, either by masking that mRNA with an antisense nucleic acid or cleaving it with a ribozyme.

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Antisense nucleic acids are DNA or RNA molecules that are complementary to at least a portion of a specific mRNA molecule. In the cell, they hybridize to that mRNA, forming a double stranded molecule. The cell does not translate an mRNA in this double-stranded form. Therefore, antisense nucleic acids interfere with the expression of mRNA into protein. Oligomers of about fifteen nucleotides and molecules that hybridize to the AUG initiation codon will be particularly efficient, since they are easy to synthesize and are likely to pose fewer problems than larger molecules upon introduction to cells.

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This invention provides a transgenic nonhuman mammal which comprises the isolated nucleic acid molecule bcl-6 introduced into the mammal at an embryonic stage.

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This invention provides an assay for non-Hodgkin's lymphoma, comprising (a) incubating a sample of suitable body fluid for a subject with a monoclonal antibody reactive with non-Hodgkin's lymphoma cells to a solid support, (b) removing unbound body fluid from the support, and (c) determining the level of antigen activity exhibited by the bound body fluid to the support.

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The suitable bodily fluid sample is any bodily fluid sample which would contain non-hodgkin lymphoma cells or fragments thereof. A suitable bodily fluid includes, but is not limited to, serum, plasma, cerebrospinal fluid, and urine. In the preferred embodiment, the suitable bodily fluid sample is serum

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or plasma. In addition, the body fluid sample may cells from bone marrow, or a supernate from a cell culture. Methods of obtaining a suitable bodily fluid sample from a subject are known to those skilled in the art.

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This invention provides a method for screening putative therapeutic agents for treatment of non-Hodgkin's lymphoma, which comprises determining in a first sample from a subject with non-Hodgkin's lymphoma the presence of the isolated nucleic acid molecule bcl-6, administering to the subject a therapeutic amount of the agent such that the agent is contacted with the cell associated with the condition, determining after a suitable period the amount of the isolated nucleic acid molecule in a sample from the treated subject, and comparing the amount of isolated nucleic acid molecule determined in the first sample with the amount determined in the sample from the treated subject, a difference indicating the effectiveness of the agent, thereby screening putative therapeutic agents for treatment of non-Hodgkin's lymphoma.

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Further, this invention provides an assay system that is employed to identify drugs or other molecules capable of binding to the nucleic acid molecule bcl-6 or proteins, either in the cytoplasm or in the nucleus, thereby inhibiting or potentiating transcriptional activity. Such assay would be useful in the development of drugs that would be specific against particular cellular activity, or that would potentiate such activity, in time or in level of activity.

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The above described probes are also useful for in-situ hybridization or in order to locate tissues which express this gene, or for other hybridization assays for the presence of this gene or its mRNA in various

biological tissues.

The in-situ hybridization technique using the labelled nucleic acid molecule bcl-6 is well known in the art.
5 Essentially, tissue sections are incubated with the labelled nucleic acid molecule to allow the hybridization to occur. The molecule will carry a marker for the detection because it is "labelled", the amount of the hybrid will be determined based on the
10 detection of the amount of the marker. Further, immunohistochemical protocols may be employed which are known to those skilled in the art.

This invention provides a method of diagnosing diffuse-type B-cell lymphoma in a subject which comprises
15 detecting in a sample from the subject nucleic acid molecule of bcl-6 locus.

This invention provides a method for diagnosing B-cell lymphoma in a subject comprising: (a) obtaining DNA
20 sample from the subject; (b) cleave the DNA sample into fragments; (c) separating the DNA fragments by size fractionation; (d) hybridizing the DNA fragments with a nucleic acid molecule comprising a nucleic acid
25 molecule of at least 15 nucleotides capable of specifically hybridizing with a sequence included within the sequence of the nucleic acid molecule of the bcl-6 locus to detect the DNA fragment containing the bcl-6 sequence; and (e) comparing the detected DNA
30 fragment from step (d) with the DNA fragment from a known normal subject, the difference in size of the fragments indicating the occurrence of B-cell lymphoma in the subject. In a preferred embodiment, the above diagnostic method is for diffuse-type B-cell lymphomas.

35 A person of ordinary skill in the art will be able to obtain appropriate DNA sample for diagnosing B-cell

lymphoma in a subject. The DNA sample obtained by the above described method may be cleaved by restriction enzyme. The uses of restriction enzymes to cleave DNA and the conditions to perform such cleavage are well-known in the art.

In an embodiment, the size fractionation in step (c) of the above-described method is effected by a polyacrylamide gel. In another embodiment, the size fractionation is effected by an agarose gel.

This invention also provides the above-described diagnosis method wherein step the nucleic acid molecule in step (d) is labeled with a detectable marker. The detectable marker includes but is not limited to a radiolabelled molecule, a fluorescent molecule, an enzyme, or a ligand.

In a preferred embodiment, the above-described diagnosis method further comprises transferring the DNA fragments into a solid matrix before the hybridization step (d). One example of such solid matrix is nitrocellulose paper.

As an example for the above-described diagnosis method is shown in Figures 4A-4C where different NHL sample are analyzed. More lymphoma cases and their breakpoints are shown in Figure 6.

This invention also provides a method for diagnosing B-cell lymphoma in a subject comprising: (a) obtaining RNA sample from the subject; (b) separating the RNA sample into different species by size fractionation; (c) hybridizing the RNA species with a nucleic acid molecule comprising a nucleic acid molecule of at least 15 nucleotides capable of specifically hybridizing with a sequence included within the sequence of the nucleic

acid molecule of the bcl-6 locus to detect the RNA species containing the bcl-6 sequence; and (d) comparing the RNA species obtained from (c) with the RNA species from a known normal subject, the difference
5 in size of the species indicating the occurrence of B-cell lymphoma in the subject.

In an embodiment, the size fractionation in step (b) is effected by a polyacrylamide or agarose gel.
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This invention also provides the above-described method where in step (c), the nucleic acid molecule is labeled with a detectable marker. The detectable marker includes but is not limited to a radiolabelled
15 molecule, a fluorescent molecule, an enzyme, or a ligand.

This invention also provides the above-method further comprises transferring the RNA species into a solid matrix before step (c).
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This invention also provides various uses of bcl-6 locus/gene and its derivatives. This invention further provides a method for diagnosis of B cell lymphoma and/or diffuse-type B cell lymphoma using bcl-6 DNA
25 probes or synthetic oligonucleotide primers derived from bcl-6 sequences to detect bcl-6 rearrangements/mutations by Southern blotting PCR or other DNA based techniques.

This invention also provides a method of diagnosis of B cell lymphoma and/or diffuse-type B cell lymphoma using bcl-6 DNA probes or synthetic oligonucleotide primers derived from bcl-6 sequences to detect abnormal
35 bcl-6 RNA species by Northern blotting, PCR or other RNA-based techniques.

This invention further provides a method of diagnosis of B cell lymphoma and/or diffuse-type B cell lymphoma using antiserum or monoclonal antibodies directed against the bcl-6 protein product(s).

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This invention provides a method of treating a subject with non-Hodgkin's lymphoma comprising administering an effective amount of the antisense molecule of the nucleic acid molecule bcl-6 operatively linked to a suitable regulatory element coupled with a therapeutic DNA into a tumor cell of a subject, thereby treating the subject with non-Hodgkin's lymphoma.

15

This invention provides a method of treating a subject with non-Hodgkin's lymphoma, comprising administering an effective amount of the antagonist capable of blocking the expression of the polypeptide encoded by the isolated nucleic acid molecule of bcl-6, and a suitable acceptable carrier, thereby treating the subject with non-Hodgkin's lymphoma.

20

Further, as is known to those of ordinary skill in the art effective amounts vary with the type of therapeutic agent. It is known to those of ordinary skill in the art how to determine an effective amount of a suitable therapeutic agent.

25

The preparation of therapeutic compositions which contain polypeptides, analogs or active fragments as active ingredients is well understood in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions, however, solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared. The preparation can also be emulsified. The active therapeutic ingredient is often mixed with excipients which are pharmaceutically acceptable and

30

35

compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the composition can
5 contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents which enhance the effectiveness of the active ingredient.

10 A polypeptide, analog or active fragment can be formulated into the therapeutic composition as neutralized pharmaceutically acceptable salt forms. Pharmaceutically acceptable salts include the acid addition salts (formed with the free amino groups of
15 the polypeptide or antibody molecule) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed from the free carboxyl groups can also be
20 derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

25 The subjects contained herein may be a mammal, or more specifically a human, horse, pig, rabbit, dog, monkey, or rodent. In the preferred embodiment the subject is a human.

30 The compositions are administered in a manner compatible with the dosage formulation, and in a therapeutically effective amount. Precise amounts of active ingredient required to be administered depend on
35 the judgment of the practitioner and are peculiar to each individual.

Suitable regimes for initial administration and booster shots are also variable, but are typified by an initial administration followed by repeated doses at one or more hour intervals by a subsequent injection or other administration.

As used herein administration means a method of administering to a subject. Such methods are well known to those skilled in the art and include, but are not limited to, administration topically, parenterally, orally, intravenously, intramuscularly, subcutaneously or by aerosol. Administration of the agent may be effected continuously or intermittently such that the therapeutic agent in the patient is effective to treat a subject with non-hodgkin's lymphoma.

Finally, this invention provides a therapy of B cell lymphoma and/or diffuse-type B cell lymphoma using anti bcl-6 reagents including specific antisense sequences and compounds interfering with bcl-6 functions.

This invention will be better understood from the Experimental Details which follow. However, one skilled in the art will readily appreciate that the specific methods and results discussed are merely illustrative of the invention as described more fully in the claims which follow thereafter.

EXPERIMENTAL DETAIL SECTION I:

Materials and Methods

5 **DNA Extraction and Southern Blot Analysis.** Total genomic DNA was purified from frozen tumor biopsies by cell lysis, proteinase K digestion, "salting-out" purification and ethanol precipitation as previously described (11). Southern blot hybridization analysis
10 was performed in 50% formamide, 3X SSC, 10X dextran sulphate, 5X Denhardt's solution, 0.5% SDS at 37°C for 16 hrs. Filters were washed in 0.2X SSC, 0.5% SDS at 60°C for 2 hrs. DNA probes were ³²P-labelled by the random priming method (12).

15 **DNA Probes.** The following probes were used for Southern blot analysis of Ig gene rearrangements: i) (J_H) probe: 6.6 kb *Bam*HI/*Hind*III fragment from the human Ig heavy-chain (Ig_H) locus (13); ii) (C_μ) probe:
20 1.3 kb *Eco*RI fragment containing the first two exons of human C_μ (13).

Genomic Cloning. Genomic libraries from NHL cases SM1444 and KC1445 were constructed by partial *Sau* 3A
25 restriction digestion of genomic DNA and ligation of gel-purified 15-20 kb fractions into LambdaGem-11 phage vector (Promega). Library screening was performed by plaque-hybridization using the C_μ probe.

30 **Fluorescence in situ Hybridization Analysis (FISH).** Phage DNA was labelled with biotin-14-dATP by nick translation and hybridized to metaphase spreads from normal human lymphocytes as described (14). To
35 visualize the hybridization signal and the corresponding bands sequentially under the microscope, the slides were stained and counterstained with propidium iodide and 4'6'-diamideno-2-phenylindole

(DAPI), respectively.

Northern Blot Hybridization Analysis. RNAs from several human cell lines were extracted by the guanidine-isothiocyanate method (15). For Northern blot analysis, RNA samples were electrophoresed through 0.9% agarose-2.2M formaldehyde gels and then transferred to nitrocellulose filters. Hybridization and washing were performed as described for Southern blot analysis.

Experimental Results:

DNA was extracted from tumor tissue of two cases (SM1444 and KC1445) of IgM-producing, diffuse-type B-cell NHL carrying the t(3;14)(q27;q32) translocation. Since the involvement of the Ig_H locus was suspected based on the 14q32 breakpoint, SM1444 and KC1445 DNAs were first analyzed by Southern blot hybridization using combinations of enzymes and probes specific for the J_H and C_μ regions of the Ig_H locus (13). In both cases, digestion by BamHI showed rearranged fragments containing J_H sequences (Figure 1). Subsequent hybridizations to the C_μ probe showed, in each case, that one rearranged fragment containing J_H sequences was not linked to C_μ sequences (see failure of the C_μ probe to hybridize to the same rearranged BamHI fragment detected by J_H (Figure 1) as would be expected for the physiologically rearranged Ig_H allele in IgM producing cells. In addition, in both cases, digestion with HindIII and hybridization with C_μ detected a rearranged fragment, a finding inconsistent with either germ-line or physiologically rearranged Ig_H genes, since both HindIII sites flanking C_μ sequences are not involved in V-D-J arrangements (13). The observed pattern is, however, consistent with chromosomal breakpoints located within C_μ switch sequences, as

previously observed in several cases of chromosomal translocations involving the Ig_H locus (2,16-18).

Based on this analysis, the C_μ containing fragments
5 from each case were cloned by screening genomic
libraries constructed from SM1444 and KC1445 DNAs using
the C_μ probe. Restriction mapping and hybridization
analysis of several phage clones led to the
identification of recombinant phages from each library
10 which contained C_μ sequences linked to sequences
unrelated to the Ig_H locus (see Figure 2 for maps of
representative phage clones). The Ig portions of the
phage inserts overlapped along the C_μ region extending
5' into the switch region where alignment with the
15 restriction map of the normal Ig heavy-chain locus was
lost. The location of the breakpoint within C_μ switch
sequences was confirmed for case SM1444 by DNA sequence
analysis of the breakpoint junction of phage SM-71,
which revealed the presence of the repeated motifs
20 typical of the Ig_H switch regions on the chromosome 14
side (19). The Ig-unrelated portions of phage SM-71
and KC-51 also overlapped with each other in their
restriction maps, suggesting that they were derived
from the same genomic region. This notion is further
25 supported by the fact that probe Sac 4.0 derived from
SM-71 was able to hybridize to the corresponding region
of KC-51 in Southern blot analysis.

To determine the chromosomal origin of the Ig-unrelated
30 sequences, a recombinant phage (SM-71) derived from
case SM1444, was used as a probe in FISH analysis on
metaphase chromosome spreads from mitogen-stimulated
normal blood lymphocytes. The phage probe hybridized
specifically to chromosome 14q32 as well as to
35 chromosome 3q27 (Figure 3), indicating that the
recombinant phage insert contained one of the two
chromosomal junctions of the reciprocal t(3;14)

translocation. Thus, taken together, the results of cloning and FISH analysis established that, in both NHL cases studied, the chromosomal translocation has linked sequences within the switch region of the C_μ locus to
5 sequences from band 3q27, consistent with the cytogenetic description of the t(3;14)(q27;q32) translocation. In the two NHL cases studied, the breakpoints on 3q27 were located within 3 kb of the same genomic locus, which was termed bcl-6.

10

In order to determine whether 3q27 breakpoints in additional NHL cases were also located within the cloned portion of the bcl-6 locus, bcl-6 rearrangements were examined in a total of 19 NHL cases carrying 3q27
15 breakpoints, including 4 (two cloned cases and two additional ones) carrying t(3;14)(q27;q32) as well as 15 cases carrying 3q27 translocations involving regions other than 14q32. Southern blot hybridization using probes derived from phage SM-71 (see Figure 2) detected
20 rearranged fragments in EcoRI-and/or BglIII-digested DNA in 7 of 19 cases studied, including all 4 t(3;14) cases as well as 3 cases with other types of translocations (see Figures 4A-4C for cytogenetic description of the cases and representative results). These results
25 indicate that heterogeneous 3q27 breakpoints cluster in a fairly restricted region within bcl-6 independently of the partner chromosome involved in the translocation.

30 Whether the bcl-6 locus adjacent to the chromosomal breakpoints contained a transcriptional unit was investigated. Probe Sac 4.0 (see Figure 2) was used to detect RNA expression in several human cell lines by Northern blot analysis. A major 2.4 kb RNA species was
35 readily detectable in two B-cell derived cell lines tested, while a relatively less abundant 4.4 kb species is present in CB33 only. No hybridization was detected

in a T-cell derived cell line (HUT 78) nor in HeLa cells (Figure 5). This result indicates that 3q27 sequences immediately adjacent to the chromosomal breakpoint cluster are part of a gene (bcl-6) which is expressed in cells of the B lineage.

Experimental Discussion:

This study reports the identification and cloning of a genomic region, bcl-6, involved in recurrent chromosomal translocations affecting band 3q27 in NHL. The region is defined by the clustered position of breakpoints in seven NHL cases carrying 3q27 translocations involving either IgH or several other loci. A more precise definition of the bcl-6 locus and of the frequency of its involvement in NHL requires cloning and characterization of additional bcl-6 sequences and studying additional tumor cases. Nevertheless, the finding that various translocation partner chromosomes have been joined to the same region on chromosome 3 in cytogenetically heterogeneous NHL cases supports the notion that rearrangement of the bcl-6 locus may represent the critical common denominator of translocations involving 3q27.

The second finding of this study is that the bcl-6 locus contains a gene which is expressed in B-cells. It is not clear at this stage whether the chromosomal breakpoints directly truncate coding or regulatory sequences of bcl-6, or, whether the gene remains intact with its regulation overridden by transcriptional control motifs juxtaposed by the translocation. The clustering of breakpoints in the seven studied NHL cases suggests, however, that bcl-6 may be a proto-oncogene which can contribute to NHL pathogenesis upon activation by chromosomal translocation. Results of this study will allow elucidation of the normal

structure and function of the bcl-6 gene in order to understand the pathogen consequences of chromosomal translocation of bcl-6 and its role in lymphomagenesis.

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EXPERIMENTAL DETAIL SECTION II

Introduction:

- 5 The molecular analysis of specific chromosomal translocations has improved the understanding of the pathogenesis of non-Hodgkin lymphoma (NHL), a heterogeneous group of B-cell or, less frequently, T-cell malignancies (1,2). The (14;18) chromosomal
- 10 translocation, which causes the deregulated expression of the anti-apoptosis gene BCL-2, plays a critical role in the development of follicular lymphoma (FL) (3-6), which accounts for 20 to 30% of all NHL diagnoses (7). Burkitt's lymphoma (BL) and mantle-cell lymphoma, two
- 15 relatively rare NHL types, are characterized by chromosomal translocations causing the deregulated expression of the cell-cycle progression genes C-MYC and the BCL-1/cyclin D1, respectively (8-15).
- 20 Relatively little is known about the molecular pathogenesis of diffuse large cell lymphoma (DLCL), the most frequent and most lethal human lymphoma (7). DLCL accounts for ~40% of initial NHL diagnoses and is often the final stage of progression of FL(7). A small
- 25 percentage of DLCL display C-MYC rearrangements (16) and 20 to 30% display alterations of BCL-2 reflecting the tumor's derivation from FL (17). However, no consistent molecular alteration has been identified that is specific for DLCL.
- 30 Chromosomal translocations involving reciprocal recombinations between band 3q27 and several other chromosomal sites are found in 8 to 12% of NHL cases, particularly in DLCL (18-19). From NHL samples
- 35 displaying recombinations between 3q27 and the immunoglobulin (Ig) heavy chain locus on 14q32, the chromosomal junctions of several (3;14)(q27;q32)

translocations were cloned and identified a cluster of breakpoints at a 3q27 locus named BCL-6.

Experimental Results:

5 To isolate normal BCL-6 cDNA, a cDNA library constructed from the NHL cell line Bjab (22) was screened with a probe (20-21) derived from the chromosomal region flanking the breakpoints of two
10 t(3;14)(q27;32) cases. A phage cDNA library constructed from RNA of the Bjab lymphoma cell line was screened (1 X 10⁶ plaques) by plaque hybridization with the Sac 4.0 probe that had been ³²P-labelled by random priming (22). Sequence analysis (Figures 10A-10B)
15 revealed that the longest clone (3549 bp), approximately the same size as BCL-6 RNA, codes for a protein of 706 amino acids with a predicted molecular mass of 79kD. The putative ATG initiation codon at position 328 is surrounded by a Kozak consensus
20 sequence (23) and is preceded by three upstream in-frame stop codons. The 1101-bp 3'-untranslated region contains a polyadenylation signal followed by a track of poly(A). These features are consistent with BCL-6 being a functional gene.

25 The NH₂- and COOH- termini of the BCL-6 protein (Figures 10A-10B) have homologies with "zinc-finger" transcription factors (24). BCL-6 contains six C₂H₂ zinc-finger motifs (Figure 10A) and a conserved stretch
30 of six amino acids (the H/C link) connecting the successive zinc-finger repeats (25). BCL-6 can be assigned to the Krüppel-like subfamily of zinc-finger proteins. The NH₂- terminal region of BCL-6 is devoid of the FAX (27) and KRAB (28) domains sometimes seen in
35 Krüppel-related zinc-finger proteins, but it does have homologies (Figure 11) with other zinc-finger transcription factors including the human ZFPJ5

protein, a putative human transcription factor that regulates the major histocompatibility complex II promoter, the Tramtrack (ttk) and Broad-complex (Br-c) proteins in *Drosophila* that regulate developmental transcription (29), the human KUP protein (31), and the human PLZF protein, which is occasionally involved in chromosomal translocations in human promyelocytic leukemia (32). The regions of NH₂-terminal homology among ZFPJ5, ttk, Br-c, PLZF and BCL-6 also share some degree of homology with viral proteins (e.g. VA55R) of the poxvirus family (33) as well as with the *Drosophila* kelch protein involved in nurse cell-oocyte interaction (34). These structural homologies suggest that BCL-6 may function as a DNA-binding transcription factor that regulates organ development and tissue differentiation.

The cDNA clone was used as a probe to investigate BCL-6 RNA expression in a variety of human cell lines by Northern blot analysis. A single 3.8 kb RNA species was readily detected (Figure 11) in cell lines derived from mature B-cells, but not from pro-B-cells or plasma cells, T cells or other hematopoietic cell lineages. The BCL-6 RNA was not detectable in other normal other tissues, except for skeletal muscle in which low level expression was seen. Thus, the expression of BCL-6 was detected in B-cells at a differentiation stage corresponding to that of DLCL cells. This selective expression in a "window" of B-cell differentiation suggests that BCL-6 plays a role in the control of normal B-cell differentiation and lymphoid organ development.

To characterize the BCL-6 genomic locus, the same cDNA probe to screen a genomic library from human placenta was used. A phage genomic library constructed from normal human placenta DNA (Stratagene) was screened (8×10^5 plaques) with the BCL-6 cDNA. Twelve overlapping

clones spanning ~50kb of genomic DNA were isolated. After restriction mapping, the position of various BCL-6 exons was determined by Southern hybridization using various cDNA probes. By restriction mapping, hybridization with various cDNA probes, and limited nucleotide sequencing, the BCL-6 gene was found to contain at least ten exons spanning ~26 kb of DNA (Figure 12). Sequence analysis of the first and second exons indicated that they are noncoding and that the translation initiation codon is within the third exon.

Various cDNA and genomic probes were used in Southern (DNA) blot hybridizations to determine the relationship between 3q27 (Table 1). Monoallelic rearrangements of BCL-6 were detected in 12 of 17 tumors by using combinations of restriction enzymes (Bam HI and Xba I) and probe which explore ~16 kb within the BCL-6 locus. These 12 positive cases carry recombinations between 3q27 and several different chromosomes (Table 1), indicating that heterogeneous 3q27 breakpoints cluster in a restricted genomic locus irrespective of the partner chromosome involved in the translocation. Some DLCL samples (5 of 17) do not display BCL-6 rearrangements despite cytogenetic alterations in band 3q27, suggesting that another gene is involved or, more likely, that there are other breakpoint clusters 5' or 3' to BCL-6. If the latter is true, the observed frequency of BCL-6 involvement in DLCL (33%, see below) may be an underestimate.

30

Table 1.

Frequency of BCL-6 rearrangements in DLCL carrying chromosomal translocations affecting band 3q27

| | | |
|----|--|--|
| 5 | Translocation | Fraction of tumors with BCL-6 rearrangements |
| | t(3;14)(q27;q32) | 4/4 |
| 10 | t(3;22)(q27;q11) | 2/3 |
| | t(3;12)(q27;q11) | 1/1 |
| | t(3;11)(q27;q13) | 1/1 |
| | t(3;9)(q27;p13) | 0/1 |
| | t(3;12)(q27;q24) | 0/1 |
| 15 | der(3)t(3;5)(q27;q31) | 1/1 |
| | t(1;3)(q21;q27) | 1/1 |
| | t(2;3)(q23;q27) | 1/1 |
| | der(3)t(3;?)(q27;?) | 1/3 |
| 20 | Tumor samples listed in the Table were collected and analyzed for histopathology and cytogenetics at Memorial Sloan-Kettering Cancer Center. | |
| 25 | A panel of tumors not previously selected on the basis of 3q27 breakpoints but representative of the major subtypes of NHL as well as of other lymphoproliferative diseases was analyzed. Similar rearrangements were detected in 13 of 39 DLCL, but not in other cases including other NHL subtypes (28 FL, 20 BL, and 8 small lymphocytic NHL), acute lymphoblastic leukemia (ALL; 21 cases), and chronic lymphocytic leukemia (CLL; 31). These findings indicate that BCL-6 rearrangements are specific for and frequent in DLCL. In addition, the frequency of rearrangements in DLCL (33%) significantly exceeds that (8 to 12%) reported at the cytogenetic level, suggesting that some of the observed rearrangements may involve submicroscopic chromosomal alterations undetectable at the cytogenetic level. | |
| 30 | | |
| 35 | | |

All the breakpoints in BCL-6 mapped to the putative 5' flanking region, the first exon or the first intron (Figure 12). For two patients that carry (3;12)(q27;q32) translocations, the chromosomal
5 breakpoints have been cloned and precisely mapped to the first intron (SM1444) or to 5' flanking sequences (KC1445) of BCL-6 on 3q27, and to the switch region of IgH on 14q32 (20-21). In all rearrangements, the coding region of BCL-6 was left intact whereas the 5'
10 regulatory region, presumably containing the promoter sequences, was either completely removed or truncated. The resultant fusion of BCL-6 coding sequences to heterologous (from other chromosomes) or alternative (within the BCL-6 locus) regulatory sequences may
15 disrupt the gene's normal expression pattern. A BCL-6 transcript of normal size was detected by Northern blot analysis of DLCL cells carrying either normal or truncated BCL-6. Some of the truncations were in the 5' flanking sequences and would therefore not be
20 expected to generate structurally abnormal transcripts.

Experimental Discussion:

Zinc-finger encoding genes are candidate oncogenes as
25 they have been shown to participate in the control of cell proliferation, differentiation, and organ pattern formation (24). In fact, alterations of zinc-finger genes have been detected in a variety of tumor types. These genes include PLZF (32) and PML (35-38) in acute
30 promyelocytic leukemia, EVI-1 (38-39) in mouse and human myeloid leukemia, TTG-1 (40) in T-cell CLL, HTRX (41-43) in acute mixed-lineage leukemia, and WT-1 (44) in Wilm's tumor. Terminal differentiation of hematopoietic cells is associated with the down-
35 regulation of many Krüppel-type zinc-finger genes. Thus, constitutive expression of BCL-6, caused by chromosomal rearrangements, interferes with normal B-

cell differentiation, thereby contributing to the abnormal lymph node architecture typifying DLCL.

5 Given that DLCL accounts for ~80% of NHL mortality (7), the identification of a specific pathogenetic lesion has important clinicopathologic implications. Lesions in BCL-6 may help in identifying prognostically distinct subgroups of DLCL. In addition, since a therapeutic response can now be obtained in a
10 substantial fraction of cases (7), a genetic marker specific for the malignant clone may be a critical tool for the monitoring of minimal residual disease and early diagnosis of relapse (45).

15 The gene cloned from chromosomal translocations affecting band 3q27, which are common in DLCL codes for a 79 kD protein that is homologous with zinc-finger transcription factors. In 33% (13/39) of DLCL samples, but not in other types of lymphoid malignancies, the
20 BCL-6 gene is truncated within its 5' noncoding sequences, suggesting that its expression is deregulated. Thus, BCL-6 is a proto-oncogene specifically involved in the pathogenesis of DLCL.

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EXPERIMENTAL DETAIL SECTION III

Introduction:

5 Non Hodgkin's lymphoma (NHL), the most frequent tumor
occurring in patients between the ages of 20 and 40,
includes several distinct clinico-pathologic subtypes,
among which diffuse lymphoma with a large cell
component (DLCL) is the most clinically relevant in
10 terms of morbidity and mortality (1). DLCL include
intermediate-grade lymphomas with pure diffuse large-
(DLCL), or mixed small- and large-cell (MX-D)
histology, as well as high-grade immunoblastic (IMB)
lymphoma. These tumors can occur "de novo",
15 accounting for 30-40% of initial NHL diagnosis and, in
addition, can represent the final "transformation"
stage of follicular lymphomas (FL), small lymphocytic
lymphoma and chronic lymphocytic leukemia. Considered
together, "de novo" and "post-transformation" DLCL
20 account for up to 80% of NHL mortality (1).

During the past decade, abnormalities involving proto-
oncogenes and tumor suppressor genes have been
identified in association with distinct NHL subtypes
25 (2). These genetic lesions represent important steps
in lymphomagenesis as well as tumor-specific markers
which have been exploited for diagnostic and prognostic
purposes (3,4). Examples include alterations of the
MYC oncogene in Burkitt lymphoma (BL), and of the BCL-2
30 and BCL-1 oncogenes in FL and mantle-cell NHL,
respectively. With respect to DLCL, several molecular
alterations have been detected at variable frequency,
but none has been specifically or consistently
associated with the disease (2). In this invention the
35 frequency and disease-specificity of BCL-6 (5-10)
rearrangements among the principal categories of
lymphoproliferative disease, including different NHL

subtypes, acute and chronic lymphoid leukemias and multiple myeloma is demonstrated.

Materials and Methods:

5 Samples of lymphnode biopsies, bone marrow aspirates and peripheral blood were collected by standard diagnostic procedures during the course of routine clinical evaluation in the Division of Surgical
10 Pathology, Department of Pathology, Columbia University. In all instances, the specimens were collected before specific anti-tumor treatment. Diagnoses were based on the results of histopathologic, immunophenotypic and immunogenotypic analysis (11). In
15 all cases, the fraction of malignant cells in the pathologic specimen was at least 70% as determined by cytofluorimetric or immunohistochemical analysis of cell-surface markers or antigen receptor (immunoglobulin heavy chain and T cell receptor β
20 chain) gene rearrangement analysis (11).

Genomic DNA was prepared from diagnostic specimens by cell lysis, proteinase K digestion, phenol-chloroform extraction and ethanol precipitation. For Southern blot
25 analysis, 6 μ g of DNA were digested with the appropriate restriction endonuclease, electrophoresed in a 0.8% agarose gel, denatured, neutralized and transferred to Duralose filters (Stratagene, La Jolla, CA). Filters were then hybridized with the BCL-6-
30 specific Sac 4.0 probe (10) that had been 32 P-labelled by the random priming technique. After hybridization, filters were washed in 0.2X SSC (1X SSC = 0.15 M NaCl + 0.015 M sodium citrate / 0.5% sodium dodecyl sulfate) for 2 hours at 60°C and then subjected to
35 autoradiography for 24-48 hours at -80°C using intensifying screens.

All NHL cases were also analyzed for rearrangement of the BCL-2 gene using the previously described probes corresponding to the MBR and MCR regions. Immunophenotypic analysis of immunoglobulin and cell surface marker expression was performed as previously described (11).

Comparisons of histologic subsets with or without BCL-6 rearrangement were made utilizing the method of inferences from proportions (12).

Experimental Results:

The tumor panel (Table 2) used for this study is representative of the major categories of lymphoproliferative disease including NHL, 125 cases, ALL 45, CLL 51 and MM 23. The NHL series was representative of low- 41, intermediate- 45 and high-grade 24 subtypes according to the Working Formulation. Fifteen cases of cutaneous T-cell NHL were also included.

The presence of BCL-6 rearrangements was analyzed by Southern blot hybridization of tumor DNAs using a probe (Sac 4.0) (10) and restriction enzymes (BamHI and XbaI) which, in combination, explore a region of 15.2 Kb containing the 5' portion of the BCL-6 gene (first exon, 7.5 Kb of first intron and 7.4 Kb of 5' flanking sequences) (10). This region was previously shown to contain the cluster of breakpoints detected in NHL. No additional rearrangements were found using probes and restriction enzymes exploring approximately 10kb either 5' or 3' to BCL-6 sequences

The results of this analysis are summarized in Table 2 and representatively shown in Figures 13A-13B. All cases of ALL, CLL and MM showed a normal BCL-6 gene.

Eighteen of the 125 NHL cases displayed BCL-6 rearrangements. Among distinct NHL histologic subtypes, rearrangements were detected in 16/45 (35.5%) DLCL and in 2/31 (6.4%) FL ($p < .001$). One of these 2 FL cases showed both follicular and diffuse patterns of growth. Among DLCL, rearrangements were significantly more frequent in DLCL (15/33, 45.4%) than in MX-D (1/10, 10%) ($p < .01$), suggesting that these genetic lesions may be specifically associated with the diffuse large cell component of these tumors. All of the DLCL cases displaying BCL-6 rearrangements lacked BCL-2 rearrangements which were found in only two 2 DLCL cases. Although cytogenetic data were not available for the panel of tumors studied, the frequency of BCL-6 rearrangements far exceeds that expected for 3q27 aberrations (10-12% in DLCL) (8, 9), suggesting that BCL-6 rearrangements can occur as a consequence of submicroscopic chromosomal aberrations.

In order to determine whether the presence of BCL-6 rearrangements correlated with distinct immunophenotypic features of DLCL, the entire panel was analyzed for expression of immunoglobulin κ and λ light chains, and B cell-associated antigens CD19, CD20 and CD22 (11). As expected, the expression of these markers was variable in the DLCL cases tested. However, no correlation with the BCL-6 rearrangement status was found.

Table 2.
Rearrangements of the BCL-6 gene in lymphoid tumors

| | TUMOR | HISTOTYPE | REARRANGED/TESTED | % |
|----|---|------------|-------------------|----|
| 5 | | | | |
| | <u>NHL</u> | | | |
| | Low grade: | SL | 0/10 | 0 |
| | | SCC-F | 2*/18 | 11 |
| | | MX-F | 0/13 | 0 |
| 10 | | | | |
| | Intermediate grade: | | | |
| | | MX-D | 1/10 | 10 |
| | | DLCL | 15/33 | 45 |
| | | SCC-D | 0/2 | 0 |
| 15 | | | | |
| | High grade: | | | |
| | | IMB | 0/2 | 0 |
| | | SNCL | 0/22 | 0 |
| 20 | Others: | CTCL | 0/15 | 0 |
| | <u>ALL</u> | | | |
| | | B-lineage: | 0/34 | 0 |
| | | T-lineage: | 0/11 | 0 |
| 25 | | | | |
| | <u>CLL</u> | B-lineage: | 0/41 | 0 |
| | | T-lineage: | 0/10 | 0 |
| | <u>MM</u> | | 0/23 | 0 |
| 30 | NHL, non-Hodgkin's lymphoma; ALL, acute lymphoblastic leukemia; CLL, chronic lymphocytic leukemia; MM, multiple myeloma; SL, small lymphocytic; SCC-F, follicular small cleaved cell; MX-F, follicular mixed; MX-D, diffuse mixed cell; DLCL, diffuse large cell; SCC-D, diffuse small cleaved cell; IMB, immunoblastic; SNCL, small non-cleaved cell lymphoma; CTCL, cutaneous T-cell lymphoma. *: one case showed follicular and diffuse growth patterns. | | | |
| 35 | | | | |

Experimental Discussion:

In this study, BCL-6 rearrangement is established as the most frequent abnormality detectable in DLLC. Previous studies have indicated MYC and BCL-2 rearrangements detectable in 5-20% and 20% of DLLC, respectively (13). Compared to those lesions, which are also commonly associated with Burkitt's lymphoma (MYC) and FL (BCL-2), BCL-6 rearrangements appear to be more disease-specific since they were exclusively found in DLLC with the exception of 2 of 45 FL cases. Considering that one of these two FL cases displayed areas of diffuse histology, it is conceivable that BCL-6 rearrangements may be occasionally associated with atypical FL cases with mixed follicular and diffuse components. The recurrent and specific association between DLLC and structural lesions of a gene coding for a zinc finger-type transcription factor related to several known proto-oncogenes 10 suggests that these abnormalities may play a role in pathogenesis of DLCL.

Among the heterogeneous DLLC spectrum, BCL-6 rearrangements were significantly more frequent in tumors displaying a pure diffuse large cell histology (DLCL) all of which lacked BCL-2 rearrangements. Considering that DLCL can originate both "de novo" and from the "transformation" of FL, and that the latter typically carry BCL-2 rearrangements, results suggest that BCL-6 rearrangements may be specifically involved in the pathogenesis of "de novo" DLLC. This conclusion is consistent with recent findings indicating that other genetic alterations, namely the inactivation of the p53 tumor suppressor gene, may be involved in the transformation of FL to DLLC (14).

The results presented herein have relevant diagnostic and prognostic implications. DLLC represent a

heterogeneous group of neoplasms which are treated homogeneously despite the fact that only 50% of patients experience long-term disease free survival (1). The presence of a marker such as BCL-6 rearrangement identifies a sizable subset of cases with a distinct pathogenesis and, distinct biological behavior.

The pathogenesis of non-Hodgkin lymphoma with a large-cell component (DLCL, including diffuse large-cell, DLCL, diffuse mixed-cell, MX-D, and immunoblastic, IMB) is unknown. The incidence and disease-specificity of BCL-6 rearrangements in a large panel of lymphoid tumors, including acute and chronic lymphoid leukemias (96 cases), various NHL types (125 cases), and multiple myelomas (23 cases) has been tested. BCL-6 rearrangements were found in 16/45 (35.5%) DLCL, more frequently in DLCL (15/33, 45%) than in MX-D (1/10, 10%), in 2/31 (6.4%) follicular NHL, and in no other tumor types. BCL-6 rearrangements represent the first genetic lesion specifically and recurrently associated with DLCL and should prove useful for understanding the pathogenesis as well as for the clinical monitoring of these tumors.

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15 EXPERIMENTAL DETAIL SECTION IV

Introduction:

Non-Hodgkin lymphomas (NHL) represent one of the most common malignancies associated with human immunodeficiency virus (HIV) infection, and are recognized as an acquired immunodeficiency syndrome (AIDS)-defining condition (1-3). Since their initial observation in 1982 (4), the incidence of AIDS-associated NHL (AIDS-NHL) has been consistently increasing (1, 2), and they now represent the most frequent HIV-associated malignancy in some AIDS risk groups, namely the hemophiliacs (5). Indeed, some estimates project that 10 to 20% of all new NHL cases in the United States may eventually be related to AIDS (6).

AIDS-NHL are almost invariably B-cell derived NHL (1, 2, 7-12). When compared with NHL of similar histology arising in the immunocompetent host, AIDS-NHL display distinctive clinical features, including late stage at presentation, poor prognosis, and the frequent

involvement of extranodal sites (1, 2, 7-12). Systemic AIDS-NHL are histologically heterogeneous, and have been initially classified into three distinct categories, including small non cleaved cell lymphoma (SNCCCL), large non cleaved cell lymphoma (LNCCL), and large cell-immunoblastic plasmacytoid lymphoma (LC-IBPL) (7, 9). Subsequently, most investigators have agreed to classify LNCCL and LC-IBPL as a single category under the term of diffuse large cell lymphoma (DLCL).

Some progress has been made in elucidating the molecular pathogenesis of AIDS-SNCCCL (1-3). AIDS-SNCCCL is associated at variable frequency with multiple genetic lesions, including Epstein Barr virus (EBV) infection, c-MYC translocation, RAS gene family mutation, and p53 inactivation by point mutation and allelic loss (1, 3, 13-25). On the other hand, the pathogenesis of AIDS-DLCL is relatively less defined. EBV infection appears to be the only genetic lesion associated with a significant fraction of these tumors, particularly with the subset displaying plasmacytoid features, p53 lesions have not been found and c-MYC activation is restricted to a small minority of cases (1-3, 13-25).

Materials and Methods:

Pathologic samples. Biopsy samples of lymph node, bone marrow, peripheral blood, or other involved organs from forty patients with AIDS were collected during the course of standard diagnostic procedures. Thirty-two samples were derived from patients referred to the Department of Pathology, New York University, New York, NY or to the Department of Pathology, Columbia University, New York, NY. Eight samples were derived from patients referred to the Departments of Hematology

and Pathology, University of Southern California School of Medicine, Los Angeles, CA. Diagnosis was based on analysis of histopathology, immunophenotypic analysis of cell surface markers, and immunogenotypic analysis of Immunoglobulin (Ig) gene rearrangement (32). In most cases, the fraction of malignant cells in the pathologic specimen was greater than 80%, as determined by cell suspension cytofluorometric or tissue section immunohistochemical analysis of cell surface markers and by Ig gene rearrangement analysis.

DNA extraction and Southern blot analysis. DNA was purified by digestion with proteinase K, "salting out" extraction, and precipitation by ethanol (33). For Southern blot analysis (34), 6 μ g of DNA was digested with the appropriate restriction endonuclease, electrophoresed in a 0.8% agarose gel, denatured, neutralized, transferred to Duralon filters (Stratagene, LA Jolla, CA), and hybridized to probes which had been 32 P-labeled by the random primer extension method (35). Filters were washed in 0.2 X SSC (NaCl/Na citrate)/0.5% sodium dodecyl sulphate (SDS) for 2 hours at 60°C and then autoradiographed using intensifying screens (Quanta III; Dupont, Boston, MA).

DNA probes. Immunoglobulin gene rearrangement analysis was performed using a J_H probe(36) (a gift of Dr. Korsmeyer) on HindIII, EcoRI, and BamHI digests. The organization of the BCL-6 locus was investigated by hybridization of XbaI, BamHI, and BglIII digested DNA to the human BCL-6 probe Sac4.0 (26-27). In selected cases, a second probe representative of the BCL-6 locus, Sac0.8, was also used. The organization of the c-MYC locus was analyzed by hybridization of EcoRI and HindIII digested DNA to the human c-MYC locus was analyzed by hybridization of EcoRI and HindIII digested

DNA to the human c-MYC probe MC413RC, representative of the third exon of the c-MYC gene (37). The presence of the EBV genome was investigated with a probe specific for the EBV termini (5.2 Kb *Bam*HI-*Eco*RI fragment isolated from the fused *Bam*HI terminal fragment NJ-het) (38).

Experimental Results:

Forty cases of systemic AIDS-NHL were studied, including 13 SNCCL and 24 DLCL (8 LNCCL and 16 LC-IBPL). In addition, three cases of CD30+ lymphomas, which have been sporadically reported in AIDS (39), were also included. All cases displayed a predominant monoclonal B-cell population as determined by Ig gene rearrangement analysis.

Analysis of *BCL-6* rearrangements. The *BCL-6* gene contains at least 9 exons spanning approximately 26 Kb of genomic DNA (27). Sequence analysis has shown that the first exon is non-coding and that the translation initiation codon is located within the third exon (27). Rearrangements of *BCL-6* can be detected by Southern blot analysis using a probe (Sac4.0) and restriction enzymes (*Bam*HI and *Xba*I) which, in combination, explore a region of 15.2 Kb containing the 5' portion of the *BCL-6* gene (27) (Figures 14A-14C). This same region was previously shown to contain the cluster of chromosomal breakpoints detected in NHL of the immunocompetent host (27, 29). Cases showing an abnormally migrating band in only one digest were further studied by hybridizing the Sac4.0 probe to additional digests (*Bgl*III) or, alternatively, by hybridizing *Bam*HI and *Xba*I digests to a probe (Sac0.8) derived from the *BCL-6* first intron, which, being located 3' of the breakpoint cluster, explores the reciprocal chromosome 3 (Figures 14A-14C). Only cases

showing abnormally migrating bands with two restriction enzymes and/or two probes were scored as rearranged.

Rearrangements of *BCL-6* were detected 5/24 AIDS-DLCL (20.8%), both in the LNCCL (2/8; 25%) and in the LC-IBPL (3/16; 18.7%) variants (Table 3 and Figures 14A-14C). All cases of AIDS-SNCCL and CD30+ lymphomas displayed a germline *BCL-6* locus. The location of the breakpoints detected in AIDS-HNL corresponds to the pattern most commonly observed in DLCL of the immunocompetent host.

Table 3.

Frequency of *BCL-6* rearrangements in AIDS-NHL

| | SNCCL ^a | DLCL ^b | | CD30+NHL ^c |
|----|--------------------|-------------------|---------|-----------------------|
| | | LNNCL | LC-IBPL | |
| | ----- | | | |
| 20 | 0/13 | 2/8 | 3/16 | 0/3 |

^a: SNCCL, small non cleaved cell lymphoma

^b: DLCL, diffuse large cell lymphoma. The DLCL included in the panel can be further distinguished into two subgroups (LNCCL, large non cleaved cell lymphoma; and LC-IBPL, large cell immunoblastic-plasmacytoid lymphoma) as previously reported (7,9).

^c: Non-Hodgkin lymphoma expressing the CD30 cell surface antigen (39).

Other genetic lesions. The other genetic lesions investigated in the panel of AIDS-NHL included infection by EBV of the tumor clone, activation of the *c-MYC* and *RAS* proto-oncogenes, and inactivation of the *p53* tumor suppressor gene. The experimental strategies used to investigate these lesions have been described in detail elsewhere (13, 45, 40). For some of the

cases, the molecular characterization of these genetic lesions have been previously reported (13, 14, 41); for the other cases, it has been assessed in the course of this study.

5

EBV infection was assessed by Southern blot hybridization using a probe representative of the EBV termini (38) which allows to analyze clonality in EBV-infected tissues (23) (Figures 16A-16C). A monoclonal infection was detected in 5/13 (38%) SNCCCL, 17/24 DLCL (71%) [3/8 (37.5%) LNCCL and 14/16 (87.5%) LC-IBPL], and 3/3 (100%) CD30+ cases.

10

Rearrangements of c-MYC were tested by hybridizing *Hind*III and *Eco*RI digested DNAs with a probe representative of c-MYC exon 3(41) (Figures 16A-16C). Rearrangements were present in 13/13 SNCCCL (100%), 5/24 (20.8%) DLCL [2/8 (25%) LNCCL and 3/16 (18.7%) LC-IBPL], and 2/3 CD30+ cases.

15

20

Mutations of p53 and RAS were analyzed by a two step strategy. Single strand conformation polymorphism (SSCP) analysis was applied to p53 exons 5 through 9 (in 29 cases) or p53 exons 5 through 8 (in 6 cases) and to N-, K-, and H-RAS exons 1 and 2 (in 29 cases); cases displaying an altered electrophoretic pattern by SSCP were further studied by DNA direct sequencing of the PCR product. p53 mutations were scored in 8/13 (61.5%) SNCCCL, but in none of the DLCL tested (0/22). Finally, RAS activation by point mutation was positive in 3/13 (23%) SNCCCL and in 1/16 (6%) DLCL tested.

25

30

The molecular features of the cases displaying *BCL-6* rearrangements are listed in Table 4. Overall, *BCL-6* rearrangements were detected both in the presence and in the absence of clonal EBV infection of the tumor,

35

whereas c-MYC alterations and p53 mutations were consistently absent in the cases displaying BCL-6 rearrangements.

Experimental Discussion:

Diffuse large cell lymphoma (DLCL) represents the most frequent type of AIDS-NHL in the HIV-infected adult (8). Despite its epidemiologic relevance, the molecular pathogenesis of these tumors is largely unclarified (3). Analysis of the genomic configuration of *BCL-6* in a panel of AIDS-NHL indicates that *BCL-6* rearrangements are involved in approximately 20% of AIDS-DLCL, whereas they are consistently negative in AIDS-SNCCCL. In this respect, *BCL-6* rearrangements may be considered the first identified genetic lesion specific for the DLCL type among AIDS-NHL. *BCL-6* rearrangements are present in both subgroups of DLCL, i.e. LNCCCL and LC-IBPL, and occur both in the absence and in the presence of EBV infection of the tumor clone (Table 4). On the other hand, *BCL-6* rearrangements were never detected in AIDS-DLCL carrying c-MYC alterations (Table 4).

The molecular pathway leading to AIDS-SNCCCL involves c-MYC rearrangements, p53 mutations, and EBV infection in 100%, 60%, and 40% of the cases, respectively (13-26). The presence of somatic hypermutation in the immunoglobulin variable regions utilized by AIDS-SNCCCL points to chronic antigen stimulation as an additional mechanism in the development of these tumors. The second genetic pathway is associated with AIDS-DLCL, involves EBV in the large majority of cases, as well as c-MYC and/or *BCL-6* rearrangements in a fraction of cases (13-26). These distinct pathogenetic mechanisms correlate with a number of clinical features which distinguish AIDS-SNCCCL from AIDS-DLCL, including different age of onset and different CD4 counts at the time of lymphoma development (1,2,8).

Results suggest that the frequency of *BCL-6* rearrangements in AIDS-DLCL is significantly lower than that in DLCL in the immunocompetent host, where *BCL-6* rearrangements occur in more than 40% of the cases. It is possible that the genetic pathogenesis of these two groups of tumors is different, and that the molecular mechanisms active in AIDS-DLCL are characterized by a higher degree of heterogeneity. Among DLCL in the immunocompetent host, *BCL-6* rearrangements are associated with distinct clinical features, including the extranodal origin of the lymphoma and the lack of bone marrow involvement. In addition, the presence of this rearrangement appears to represent a favorable prognostic marker.

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EXPERIMENTAL DETAIL SECTION V

Introduction:

30 The group of diffuse lymphomas with a large cell component (DLCL), including diffuse mixed, immunoblastic, and large cell subtypes, and the group of follicular lymphomas, each comprise about 40 per

35 cent of non-Hodgkin's lymphomas (NHL) in this country (1). Together, the incidence of NHL is increasing at 3 to 4 per cent a year, a rate second only to that of

malignant melanoma and lung cancer in women (2). Despite significant advances in treatment, approximately half of patients with DLLC will succumb to their disease, although "high risk" individuals may successfully be treated by intensive chemotherapy and radiotherapy regimens including autologous bone marrow transplantation (3-7). The formulation of prognostic models allow clinical trials to be directed toward groups of patients with different risks for failure after conventional treatment (5).

Cytogenetic studies as well as molecular genetic analysis of alterations involving proto-oncogenes and tumor suppressor genes have provided insights into the pathogenesis of NHL, and have also contributed diagnostic and prognostic markers (8,9). Examples include rearrangements of the BCL-2 gene at 18q21 observed in up to 85 per cent of follicular lymphomas, the BCL-1 gene at 11q13 rearranged in intermediate differentiation NHL, and the MYC gene, perturbed in Burkitt's lymphoma (8,9). While no recurring genetic abnormality has been specifically associated with diffuse large cell lymphoma, rearrangement of BCL-2 has been observed in 20 to 30 per cent of cases, where it has been associated with decreased overall or disease free survival (10-12). Chromosomal translocations including those involving the MYC proto-oncogene, while noted in DLLC, were not as prognostically significant as other recurring chromosomal abnormalities (8,13).

BCL-6 (14-19) rearrangement is found to denote a subset of DLLC characterized by extranodal presentation and a favorable clinical outcome. These results indicate that, in concert with other clinical features, this molecular marker may be utilized as a prognostic indicator at the time of diagnosis.

Materials and Methods:

This study was comprised of 102 cases of DLLC studied at diagnosis with documented clonal rearrangement of the IGH gene and DNA available for further analysis, derived from 229 DLLC serially ascertained over a nine year period. Excluded were 127 cases studied at relapse, T cell DLLC, or cases for which no DNA was available. For this study, DLLC was defined as lymphomas of diffuse large cleaved, non-cleaved, immunoblastic, or mixed subtype, according to the International Working Formulation (20) as classified by a hematopathologist (DCS or DF). Cytogenetic analysis was attempted on each of the specimens as previously described (21). For detection of BCL-6 rearrangements, DNA from each case was digested with BamHI and XbaI and subjected to Southern blot analysis utilizing a 4kb SacI-SacI fragment of the BCL-6 gene as a probe (19). Cases which did not yield metaphases for karyotypic analysis were also analyzed for rearrangement of the MBR and MCR breakpoint regions of the BCL-2 gene, as previously described (11). Aggregate descriptions of 47 of the cases in the current series were included in prior reports of cytogenetic abnormalities in DLLC (11, 13, 14). A detailed molecular analysis of 8 cases (nos. 352, 755, 1098, 1254, 1403, 1444, 1445) demonstrating BCL-6 rearrangement has been reported separately (19).

For each case, clinical data were compiled as previously described (22). Stage was assessed according to the modified Ann Arbor criteria (25). For the purposes of separate evaluation of number of extranodal sites of disease, radiographs or pathologic involvement of these sites were scored. In the quantitation of extranodal sites of disease as a prognostic variable, bone marrow, but not splenic

involvement was scored, in accord with the International Prognostic Index (5).

Clinical endpoints including complete response and freedom from progression were defined as previously described (3). Of 102 patients with DLCL genetically analyzed prior to cytotoxic treatments, 93 received systemic chemotherapy. Nine patients with early stage disease were treated by surgical resection and/or radiation therapy. All patients were treated with curative intent. Chemotherapy treatments were classified into three groups: NHL-4, CHOP and BACOP (1st generation); m-BACOD, NHL-7 (2nd generation); MCOP_B, NHL-9, NHL-14, NHL-15, L-20 (3rd generation) (4,24,29). Eight patients expired before completion of therapy, with incomplete staging evaluations, or of infectious complications during or shortly after treatment. These cases were considered not valuable for the determination of remission status, but were included in the analysis of overall survival and freedom from progression. One patient was judged to be a complete remission which was confirmed by autopsy after expiration due to infectious complications 3 weeks after completion of protocol treatment. All deaths, regardless of cause were considered as endpoints in the analysis of overall survival. Median survival was determined by the method of Kaplan and Meier (30). Analysis of correlations between gene rearrangements and clinical features were performed utilizing Fisher's exact test (13). Means were compared utilizing two sample t-tests. Univariate comparisons of survival and duration free from progression were made by log rank test. Survival and freedom from progression estimates are quoted with confidence intervals (CI) given in parentheses. Multivariate analysis was performed utilizing the Cox regression model (31). Stepwise

multiple logistic regression was used in the multivariate analysis of factors prognostic for achieving a complete response. For all statistical analyses, a $P < 0.05$ based on a 2-sided test was considered significant.

Experimental Results:

Of 102 cases of DLCL studied at diagnosis, 23 demonstrated BCL-6 rearrangement, 21 demonstrated t(14;18) or rearrangement of BCL-2, and 58 demonstrated no evidence of either BCL-6 or BCL-2 rearrangement. Representative results of hybridization analysis for rearrangement of BCL-6 are depicted in Figures 17A-17B. The clinical characteristics of groups according to BCL-6 or BCL-2 rearrangement are summarized in Table 5. The histologic subtypes and clinical features of the BCL-6 rearranged cases are shown in Table 6.

The key to Table 6 is as follows: Underlining signifies site from which biopsy was performed. Histology: DLC = diffuse large cell; IMB = immunoblastic; DML = diffuse mixed lymphoma; LDH = lactate dehydrogenase in units/ml; (B) = bulky disease (> 8 cm or 1/3 thoracic diameter); CHOP = cyclophosphamide, daunorubicin, vincristine, prednisone; MACOPB = methotrexate, daunorubicin, cyclophosphamide, vincristine, prednisone, bleomycin; MBACOD = same drugs as MACOPB with dexamethasone instead of prednisone and drugs in different schedule; PrCyBom = drugs of MACOPB plus cytosine arabinoside, etoposide, methotrexate; L-20 = vincristine, cyclophosphamide, methotrexate, daunorubicin, prednisone, cytosine arabinoside, 1-asparaginase, BCNU, 6-mercaptopurine, dactinomycin; L-20 includes randomization to autologous transplantation; NHL-7 =

- CHOP plus methyl GAG, etoposide(36), NHL-14 = short course PrCyBom; NHL-15 = high dose daunorubicin, vincristine, cyclophosphamide(29); RT = radiation therapy; SURG = surgery CR = complete response; sCR = surgical complete response (all evaluable disease resected); PR = partial response; "+" = alive at last follow-up; e = expired; rel = relapse; NE = not evaluable; * = Patient 1445 had a history of low grade NHL of eyelid 7 years earlier, treated by radiotherapy. * Skin involvement of patient 252 was not noted in a prior report (14) and patient 1445 had a history of low grade NHL of eyelid 7 years earlier, treated by radiotherapy.
- 15 While each of the BCL-6 rearranged cases was classified as a DLCL, the range of morphologies included diffuse large cell (cleaved and non-cleaved), and less frequently, immunoblastic, or mixed histologies. Extensive necrosis and extranodal extension were common histologic features, and were present in one of two cases of BCL-6 rearrangement which did not show clinical evidence of extranodal disease.
- 20
- 25 The BCL-6 rearranged cases had a mean age of 64.1 years at presentation and a high frequency of extranodal involvement by disease; 19 of 23 cases had stages IE, IIE, IIIE or stage IV disease, compared to 48 of 79 of BCL-6 germline cases ($p=0.07$). Extranodal sites included muscle or subcutaneous tissues (6 cases), stomach (5 cases), lung or pleura (5 cases), skin, breast, bowel, thyroid, pancreas, or kidney, as assessed by biopsy or radiographic abnormalities which improved after chemotherapy. Of the 7 cases with state IE or IIE decrease, 5 were primary extranodal lymphomas, while 2 were extranodal extensions from a primary nodal site. Two cases were primary splenic
- 30
- 35

lymphomas. In two cases, there was only peripheral adenopathy. Compared to BCL-6 germline cases, there was no significant difference in the proportion of BCL-6 rearranged cases with stage IV disease. Bone marrow involvement was observed in 15 of 75 BCL-6 germline cases biopsied, compared to only 1 of the 23 stage IV BCL-6 rearranged cases ($P=0.1$).

All but one of the 23 patients with BCL-6 rearrangement at the time of diagnosis received anthracycline-containing chemotherapy. This patient remained free of disease eight years after resection of a primary splenic large cell lymphoma. At median follow-up in excess of two years, 21 of the 23 patients with BCL-6 rearrangement survived; the actuarial survival was 91 per cent (CI 80 per cent to 100 per cent). Two patients expired during or immediately following treatment; an autopsy in one case revealed no evidence of lymphoma. This patient, and 19 others were judged to have achieved a complete remission after treatment. Two patients relapsed with recurrent disease in the lung and two patients had persistent subcutaneous masses. One of the relapse patients (case 295) went on to autologous transplantation and remains free of disease 78 months post-transplant.

With respect to known prognostic variables, the proportion of the BCL-6 rearranged cohort with LDH > 500 U per liter was similar to the proportion of the BCL-6 germline DLLC (3/23 versus 13/79; $P=0.99$). Five of 23 cases of DLLC with BCL-6 rearrangement demonstrated bulky disease, compared to 35 of 79 cases without BCL-6 rearrangement ($P=0.1$). The proportion of cases with "limited stage" (I, IE, II, or IIE) disease was comparable in the cohorts with and without BCL-6 rearrangement (Table 5).

Table 5.

Characteristics of 102 cases of DLLC

| | BCL-6+ | BCL-6- BCL2- | BCL-6+ BCL2+ |
|---|-------------------------|------------------------|------------------------|
| 5 | | | |
| n= | 23 | 58 | 21 |
| 10 | | | |
| Mean age (years) | 64.1 | 52.7 | 62.8 |
| Mean lactate dehydrogenase (U/ml) | 405 | 331 | 389 |
| 15 | | | |
| Mean extranodal sites | 1.6 | .93 | .81 |
| Bone marrow involvement | 1/23 | 8/54 | 7/21 |
| 20 | | | |
| <u>Stage</u> | | | |
| I (IE) | 3 (1) | 3 (3) | 0 |
| II (IIE) | 7 (6) | 22 (6) | 5 |
| 25 | | | |
| III (IIIE) | 2 (1) | 8 (2) | 4 |
| IV | 11 | 25 | 12 |
| 30 | | | |
| <u>Histology</u> | | | |
| Diffuse large cell | 20 | 53 | 19 |
| Diffuse mixed | 1 | 2 | 1 |
| Immunoblastic | 2 | 3 | 1 |
| 35 | | | |
| <u>Treatment</u> | | | |
| 1st generation chemo. | 12 | 16 | 10 |
| 2nd generation chemo. | 1 | 10 | 3 |
| 3rd generation chemo. | 9 | 24 | 8 |
| other | 1 | 8 | 0 |
| 40 | | | |
| Complete Remission | 20/23 | 35/50 | 15/21 |
| Rate | 86% | 70% | 71% |
| 45 | | | |
| Projected survival at 36 months | 91% (CI 80%-100%) | 59% (CI 44%-74%) | 46% (CI 21%-72%) |
| 50 | | | |
| Projected freedom from progression at 36 months | 82% (CI 66%-98%) | 56% (CI 43%-70%) | 31% (CI 8%-53%) |

Table 6.

Clinical features of 23 cases of DLLC with BCL6 rearrangement

| CASE NUMBER | AGE/SEX | STAGE | EXTRANODAL SITES | HISTOLOGY | LDH (BULK) | TREATMENT | CLINICAL OUTCOME |
|-------------|---------|-------|---|-----------|------------|--------------|------------------|
| 102 | 66/F | IIIS | spleen | DLC | 3624 | SURG, CHOP | CR, 96+ |
| 147 | 61/F | IS | spleen | DLC | 365 (B) | SURG, RT | sCR, 101+ |
| 252 | 54/M | IV | spleen, skin [†] | DLC | 126 | MACOPB | CR, 88+ |
| 278 | 68/M | IV | pleura, iliac mass | DLC | 235 (B) | MACOPB | PR, 6e |
| 295 | 46/M | IV | lung | DLC | 179 | MACOPB, L-20 | CR, rel, 97+ |
| 352 | 53/F | IV | stomach, liver, spleen, small bowel, pleural effusion | IMB | 775 (B) | MACOPB | CR, 81+ |
| 470 | 74/F | IV | lung | DLC | 224 | CHOP | CR, 30+ |
| 534 | 70/F | IIIS | spleen, mass involving pancreas | DLC | 278 (B) | CHOP | CR, 80+ |
| 763 | 79/F | IIIE | stomach | DLC | 196 | CHOP | CR, 60+ |
| 970 | 75/M | IV | kidney, stomach | DLC | 240 | NHL-14 | CR, 4e |
| 1020 | 60/M | IIIE | tonsil, pancreas | DLC | 303 | CHOP | CR, 100+ |
| 1056 | 63/M | IIIE | stomach | DLC | 213 | SURG, MBACOD | CR, 100+ |
| 1058 | 59/M | IIIE | axillary mass involving breast | DLC | 206 | FrCyBom | CR, 37+ |
| 1098 | 74/F | IV | subcutaneous masses | DML | 181 | RT, CHOP | PR, 36+ |
| 1189 | 71/M | IV | subcutaneous masses | DLC | 330 | CHOP | PR, 21+ |
| 1254 | 74/F | IIIE | thyroid | DLC | 196 | CHOP/RT | CR, 27+ |
| 1264 | 76/F | IV | lung, liver, spleen, kidney | DLC | 234 | CHOP | CR, rel, 27+ |
| 1299 | 50/M | IE | deloid mass, bone | DLC | 529 (B) | FrCyBom | CR, 16e |
| 1363 | 47/M | III | NONE | DLC | 129 | NHL-15 | CR, 16+ |
| 1403 | 62/M | I | NONE | IMB | 222 | CHOP, RT | CR, 11+ |
| 1407 | 71/M | IIIE | stomach | DLC | 206 | SURG, CHOP | CR, 12+ |
| 1444 | 70/F | IV | lung | DLC | 150 | CHOP | CR, 14+ |
| 1445 | 63/F | IV | neck mass involving muscle, bone marrow | DLC | 174 | NHL-15 | CR, 8+ |

Multivariate analysts of clinical outcome. The median duration free from progression of disease was not reached in the BCL-6 rearranged DLCL compared to 70 months for BCL-6 germline cases, regardless of BCL-2 status ($P=0.009$) (Figure 18A). Projected freedom from progression at 36 months was 82% (CI 66%- 98%) and 49% (CI 37%-60%), respectively. Multivariate analysis revealed that four variables, BCL-6 status, stage IV disease, bulk of disease, and LDH (log transformed) were the most powerful prognostic indicators for freedom from progression (Table 7). Multivariate analysis of survival demonstrated that bulk, LDH, BCL-6 status, and stage IV disease were the most useful predictors of overall survival ($P=0.01$, $P=0.02$, $P=0.02$, $P=0.05$, respectively).

Table 7

Multivariate analysis of freedom from progression

| | Variables selected into Cox regression model | Relative Risk | P value (Wald chi square) |
|----|--|-------------------|------------------------------|
| 30 | BCL-6 rearranged | 0.18 (CI .04-.78) | 0.007 |
| | Bulky disease | 2.4 (CI 1.3-7.4) | 0.01 |
| | Stage IV disease | 2.1 (CI 0.98-5.2) | 0.03 |
| 35 | LDH (log transformed) | 1.6 (CI 1.1-3.9) | 0.05 |

The prognostic value of BCL-6 gene status was compared to risk variables calculated according to the International Prognostic Index³, including serum LDH level, stage, performance status, and number of extranodal sites. A cox regression analysis confirmed

the independent prognostic value of BCL-6 gene status; patients with BCL-6 rearrangement had a relative risk (RR) of dying of .09 (CI .02 to .42) compared to patients without BCL-6 rearrangement, controlling for
5 the other prognostic variables in the model ($P=0.002$).

When cases were considered with respect to BCL-2 status, the BCL-2 rearranged cases demonstrated a trend for a decreased survival compared to BCL-2
10 germline cases, regardless of BCL-6 status ($P=0.12$). When BCL-6 and BCL-2 status were considered together (Figure 18B), BCL-6 rearranged cases demonstrated a projected actuarial survival at 36 months of 91% (CI 80%-100%) compared to 59% (CI 44%-74%) for the BCL-6
15 germline/BCL-2 germline cohort, and 46% (CI 21%-72%) for the BCL-2 rearranged cohort. While the logrank test between these three cohorts demonstrated a difference in survival ($P=0.02$, Figure 18B), the major factor driving the significant summary P value was the
20 better survival of the BCL-6 rearranged cohort. The projected freedom from progression at 36 months was 82% (CI 66%-98%), 56% (CI 43%-70%) and 31% (CI 8%-53%) for the three groups. Median follow-up for survivors was two years. BCL-2 rearrangement did not emerge as
25 an independent prognostic marker in the multivariate analysis of survival or freedom from progression.

There was also no prognostically significant effect of generation of chemotherapy treatment on survival, or
30 freedom from progression ($P=0.95$, 0.21 , respectively). There was a trend for a higher complete response rate among the BCL-6 rearranged cohort (Table 5, $P=0.1$), although logistic regression revealed that only the clinical parameters LDH, stage IV, and bulk of disease
35 were independent predictors of response.

Relationship between BCL-6, BCL-2, and 8q24

rearrangements. Of the 79 cases which lacked BCL-6 rearrangement, 21 demonstrated t(14;18)(q32;q21) or rearrangement of BCL-2 by molecular analysis. These cases were characterized by an older age at diagnosis, but were similar to the larger cohort of BCL-2 negative, BCL-6 negative cases with respect to LDH, and distribution of histologies (Table 6).

Nine cases of DLCL demonstrated t(8;14)(q24;q32). Three of these biopsies were from extranodal sites including liver, bone and soft tissue. Two additional cases were splenic lymphomas. In two cases, t(8;14) bearing DLCL also demonstrated BCL-6 rearrangement. There was no impact on survival of the t(8;14) in DLCL with or without BCL-6 rearrangement. The two cases of t(8;14) with co-incident BCL-6 rearrangement did not show evidence of histologic transformation or other unusual histologic features. One of these cases (no. 147) was the single case treated by splenectomy and radiation therapy alone. The second case was the single BCL-6 rearranged case successfully salvaged by autologous transplantation.

Cytogenetic features, including the relationship between 3q27 and BCL-6 rearrangement. Of the 65 DLCL with karyotypic abnormalities, 14 demonstrated translocations and one a deletion affecting band 3q27; only 11 among these 15 cases showed rearrangement of BCL-6. Five cases with apparently normal chromosomes demonstrated BCL-6 rearrangements by DNA analysis.

Experimental Discussion:

As a group, DLLC are among the most common forms of NHL seen in this country (1). These tumors have not, however, been associated with a characteristic genetic abnormality (8). Seen in the vast majority of follicular lymphomas, t(14;18)(q32;q21) or its molecular equivalent, BCL-2 rearrangement, have been observed in 20 to 30 per cent of DLLC (8). In such cases, the t(14;18) may reflect a follicular origin of these tumors. The recognition of translocations involving 3q27 and the sites of IG genes, 14q32, 22q11, and 2p12, in predominantly diffuse NHL led to the molecular cloning of BCL-6 (14-19). While not unique to diffuse large cell lymphomas, translocations affecting 3q27 were observed only in 7 of > 200 cases of follicular NHL with abnormal karyotype reported in catalog of chromosome abnormalities in cancer (32). Of 28 cases of follicular NHL analyzed in a prior study, none demonstrated rearrangement of BCL-6 (19). BCL-6 rearrangement was established as the most common genetic lesion specific to DLLC at the time of diagnosis.

Unlike 18q21 translocations in NHL which, to date only have involved IG gene loci as reciprocal partners, 3q27 translocations demonstrated a marked promiscuity of rearrangement partners. In addition to the sites of the IG genes, reciprocal translocations involving the 3q27-29 region with at least 12 other loci; a total of 79 DLLC with 3q27 translocations has been demonstrated.

Since 4 tumors in the current series with documented 3q27 aberrations did not reveal BCL-6 rearrangement with the probe used in this study, the true frequency of BCL-6 rearrangement in DLLC at diagnosis may be

higher than the 23 per cent rate reported here. Additional breakpoints may be documented outside the recognized break cluster region of BCL-6 (19), in neighboring genes such as EV-1 (34), or in other genes not yet described. Such molecular heterogeneity is not unique in NHL; seemingly identical chromosomal translocations have been shown to demonstrate a diversity of breakpoints possibly involving different genes (35).

The frequent occurrence of BCL-6 rearrangement in DLCL characterized by extranodal involvement represents one of the few genetic markers for this subset of lymphoma (8). Rearrangements of BCL-1, BCL-2, or BCL-3 have been documented infrequently in extranodal lymphomas (36-38), while 5 of 12 gastric lymphomas in one series demonstrated MYC (8q24) rearrangement (38). The current series did not confirm the association between 8q24 rearrangement and gastric lymphoma, although t(8;14) was seen in five cases of extranodal lymphoma, one of which also showed BCL-6 rearrangement. The proportion of BCL-6 rearranged cases with stages IE, IIE, IIIE, or IV disease was higher than the proportion of BCL-6 germline DLCL; in the latter group, stage IV disease was more commonly due to bone marrow involvement. Whether this association with extranodal involvement of disease reflects an effect of the primary deregulation of BCL-6 or "secondary" genetic events associated with tumor progression (8,21) is unclear. The observation of t(3;22), t(2;3), or t(3;14) as solitary cytogenetic abnormalities in some tumors (14,15), is consistent with a primary pathogenetic role for this translocation.

While this analysis and two other reports did not confirm the very short survival of BCL-2 rearranged

DLLC initially reported (10, 12, 13, 39), the BCL-2 rearranged DLLC did demonstrate a trend for a poorer overall survival. The finding of a favorable prognosis for the subset of stage IE-IIIE extranodal
5 DLLC with BCL-6 rearrangement is consistent with prior reports of a good prognosis associated with localized extranodal large cell NHL treated with surgery or radiotherapy (40). Extranodal involvement in advanced stage disease, noted in the majority of the BCL-6
10 rearranged cases, has generally been considered a poor prognostic factor in large series of DLLC, although the negative impact of this feature was most evident when combined with other adverse indicators such as bulk, high LDH, or low performance status (5, 22, 41).
15 In contrast, bone marrow involvement, observed in 22 percent of DLLC, and considered an extranodal site in the International Prognostic Index (5), was rare in the BCL-6 rearranged cohort. The favorable treatment outcome of the BCL-6 cohort, must also be tempered by
20 the observation of relapse or residual disease in 3 of the patients still alive. An additional relapse case remains in remission 6 years after "salvage" autologous transplantation.

25 The BCL-6 rearranged cohort of DLLC also possessed other clinical markers of favorable prognosis; although comparable with respect to LDH and proportion with stage I-IIIE disease, the proportion of cases
30 with bulky disease or bone marrow involvement was lower in the BCL-6 rearranged cohort. Multivariate analysis suggested, however, that BCL-6 gene rearrangement added independent prognostic power when analyzed together with clinically-derived variables of the International Prognostic Index (5). This
35 observation is illustrated by case 352, which displayed both BCL-6 rearrangement as well as clinical features consistent with a high level of risk in the

International Index (elevated LDH, extensive extranodal involvement, low performance status, and stage IV disease), but who attained a durable remission.

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Because of issues of toxicity versus efficacy of autologous bone marrow transplantation or peripheral stem cell rescue, the identification of both favorable and unfavorable prognostic markers offers the potential to stratify treatment approaches to DLCLC based on risk groups (4-7, 22, 41). The probability of treatment failure remains as high as 25-40 per cent for the most favorable subsets of DLCLC based on current prognostic models, highlighting the need for genetic or other prognostic markers (5). In addition to its potential diagnostic and prognostic applications, the further identification of BCL-6 breakpoint regions offers the opportunity to develop new polymerase chain reaction-derived measures of minimal residual disease (43). The availability of BCL-6 rearrangement as a new molecular marker of large cell lymphoma constitutes a potentially important clinical tool in the management of patients with this disease.

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